

FIG. 1A

GAA	CAC	CCC	CTC	TTT	GGC	TGC	CTG	CGC	AGC	CCC	CAC	GGC	ACA	GCG	CAA	GGC	TTG	CAC	CCC	TTC	TGC	CAG	TCT	TCT	274
E	H	P	L	F	G	C	L	R	S	P	H	A	T	A	Q	G	L	H	P	F	S	Q	S	S	26
CTG	GGC	CTC	CAT	GGA	AGA	TCT	GAC	CAC	ATG	TCG	TCC	ACA	TCT	TCG	TCT	TGC	ATA	ATC	GGG	349					
L	A	L	H	G	R	S	D	H	M	Y	P	E	L	S	T	S	S	C	I	I	A	51			
GGA	TAC	CCC	AAT	GAG	GAG	GGC	ATG	TTT	GGC	AGC	CAG	CAT	CAC	AGG	GGG	CAC	CAC	CAC	CAC	CAC	CAT	424			
G	Y	P	N	E	E	G	M	F	A	S	Q	H	H	R	G	H	H	H	H	H	H	H	76		
CAC	CAC	CAG	CAG	CAG	CAG	CAG	GCT	CTG	CAA	AGC	AAC	TGG	CAC	CTC	CCG	CAG	ATG	TCC	TCC	CCG	CCA	AGC	499		
H	H	H	Q	Q	H	Q	A	L	Q	S	N	W	H	L	P	Q	H	S	P	P	S	101			
GCG	GCG	CGG	CAC	AGC	CTT	TGC	CTG	CAG	CCT	GAT	TCC	GGG	CCC	CCC	GAG	CTG	GGG	AGC	AGC	CCT	CCG	GTC	CTC	574	
A	A	R	H	S	L	C	L	Q	P	D	S	G	G	G	P	P	E	L	G	S	S	P	V	L	126
TGC	TCC	AAC	TCT	TCT	AGC	CTG	GGC	TCC	AGC	ACC	CCC	GGG	GGC	GGC	TGC	GCA	AGG	GAT	TAT	GTC	CCT	CAA	649		
C	S	N	S	S	L	G	S	T	P	T	G	A	A	C	A	P	R	D	Y	G	R	Q	151		
GCG	CTG	TCA	CCC	GCA	GAA	GTG	GAG	AAG	AGA	AGT	GGC	AGC	AAA	AGA	AAA	AGC	GAC	AGT	TCA	GAT	TCC	CAG	GAA	GGG	724
A	L	S	P	A	E	V	E	K	R	S	G	S	K	R	K	S	D	S	D	S	Q	E	G	176	
AAT	TAC	AAG	TCA	GAA	GTG	AAC	AGC	AAA	CCT	AGG	AAG	GAA	AGA	ACA	GCT	TTC	ACC	AAA	GAG	CAA	ATG	AGA	GAA	CTT	799
N	Y	K	S	E	V	N	S	K	P	R	K	E	R	(1)	A	F	T	K	E	Q	I	R	E	L	201
GAG	GCA	GAG	TTC	GGC	CAT	CAT	AAC	TAT	CTG	ACC	AGA	CTG	AGA	AGA	TAT	GAG	ATA	GCG	GTG	AAC	CTA	GAC	CTC	ACT	874
E	A	E	F	A	H	H	N	Y	L	T	R	L	R	Y	E	I	A	V	N	L	D	L	(T)	220	

MATCH TO FIG. 1B

MATCH TO FIG. 1A

GGAGTGTGCTAAATATTAAACGCCGGCAACTCAAGTCGTCTTCTATGTTGATAAGGGTTACACTAAGGCTCTTATTTGAAGATGCTCCAC
AGTGAATTGGAGAACATCTAAATATACTTGTCTTATATGACAGAGGGAGATGAATGTTGGCTTGCACGTGAAAATTAATTTG
CTACCAAGAGCAAACCTCGGTAAGACAATTTGACTCAAGTGTCCAGAGTGAAGATGTTATAGAAATGCTTGGACATTCCAGTTGACCGTCAATGTT
GTGTGACACTGGGCAGGTATTGGCTTTGCTTGACTGAACTAACTGCTATCAAGGTTACCAACTAACTGCTTAACTCTAAGTCATTTAGCAAAATGCACTTCAATTAGC
AAATACCCAAAGTGGATAAAAATGAACTGAAAATTCGTATATTACTCTIAAGTCATTTCCTGCTTCACTAAATTAGCAAAATGCACTTCAATTAGC
TGTGAAAAATAGGCCTTCCCCTGAGACAAATGGCAGCCAGCTCTGTGTTATACATTTCAGAGCATCAGTAGTGTGCTTACTTGTGTT
TAGAGTGGAAAATGCACTAGAGTCGTAGGGACATATTCTGGTACCAAGACAAAAACAAATCTCTGTTGCACTGACTATCAACTGTGAGATACTAT
CAGATGCTGATTGTAACCTTAACTGTTAACTGTTATGGTATGTTGACTTCTCATTGTTTATGATACAAAACCCA
AGTGCACACACCTAGCCCCCTCCAGGCCCTCTGAAAGACATTAGCGTCAAGGCAAGTAGTGTACCTTGCCAAATGAGTCTTGTTGG
ATGCCAAACAAAGCTAGTCTCTGTTAAAGGGATAGATGAGAACACTGAATGCTGACAAGTAGACTCAGGAAAATACATTATTTICAGGGCTGGTGTATTC
ATGCCAAACAAAGCTAGTCTCTGTTAAAGGGATAGATGAGAACACTGAATGCTGACAAGTAGACTCAGGAAAATACATTATTTICAGGGCTGGTGTATTC

三

四

Nmyc-1	■ □	□ ■	□ ■	□ ■	□ ■
Lamb-1	■ □	■ □	■ □	■ □	■ □
Gax	■ □	■ □	■ □	■ □	■ □
D12Nyul	■ □	■ □	■ □	■ □	■ □
Spnb-1	■ □	■ □	■ □	■ □	■ □
	50 57	10 6	4 5	6 4	6 13

FIG. 2

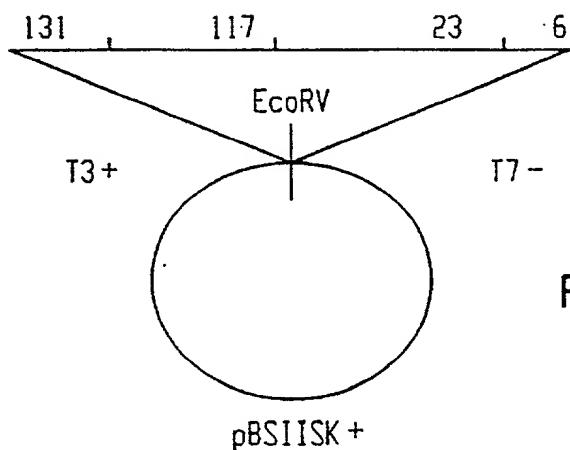
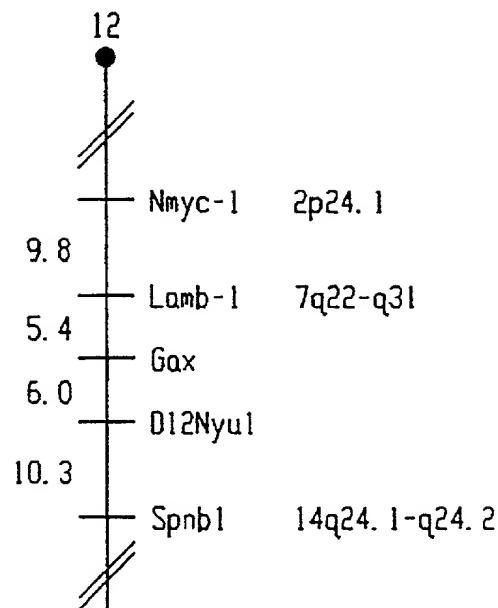


FIG. 4

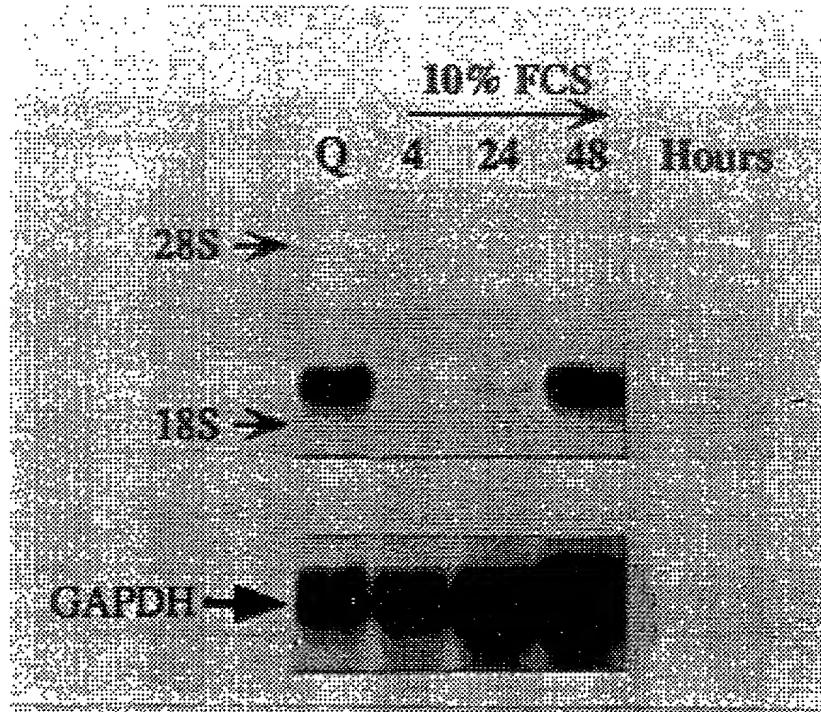


FIG. 5A

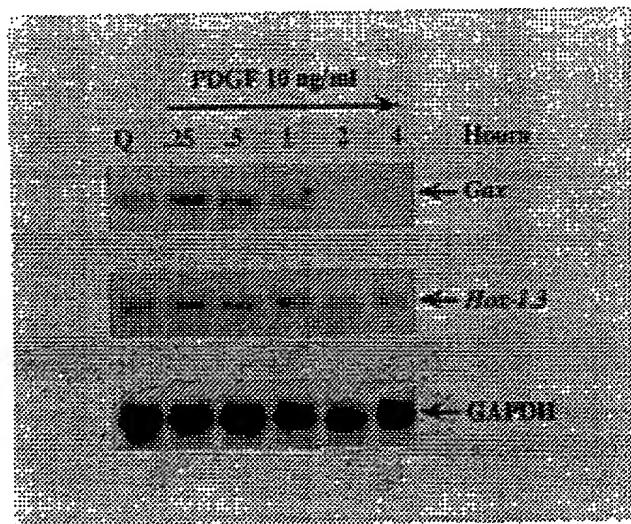


FIG. 5B

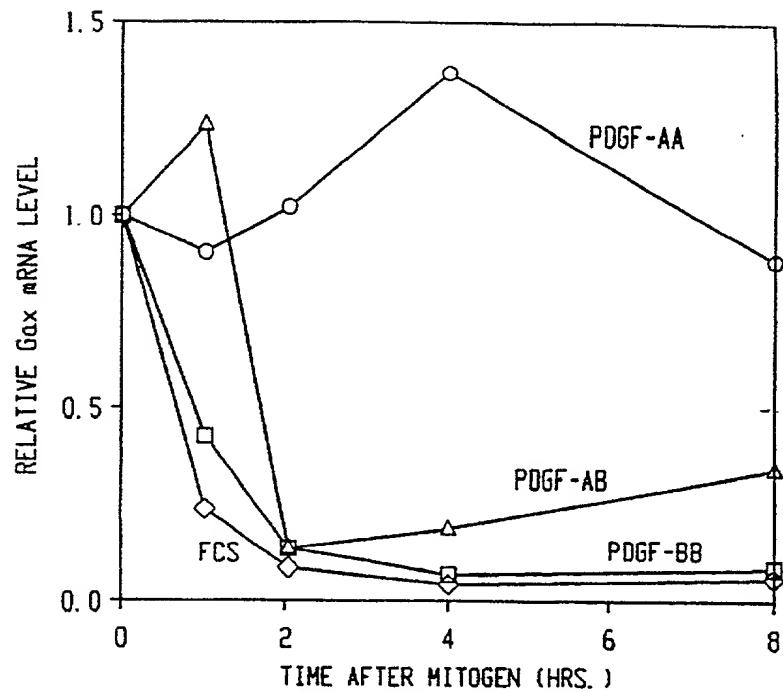


FIG. 6

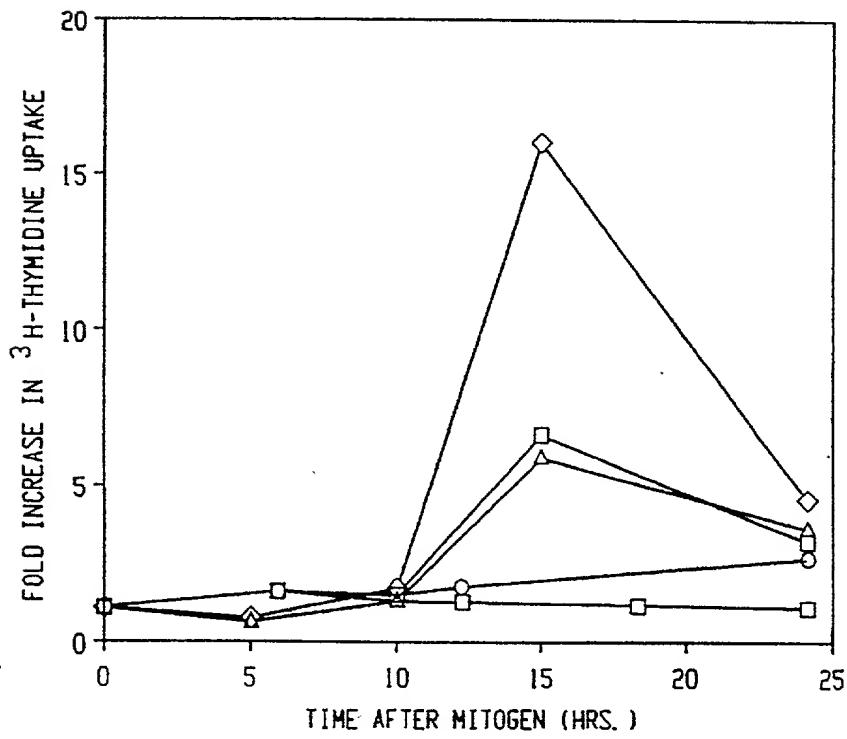


FIG. 7

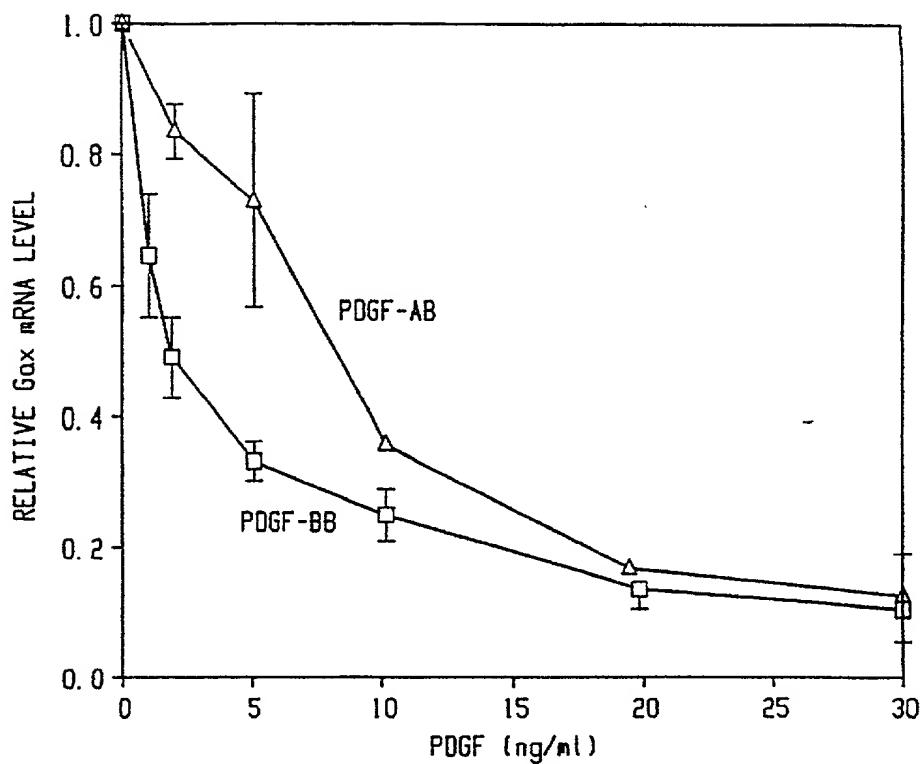


FIG. 8

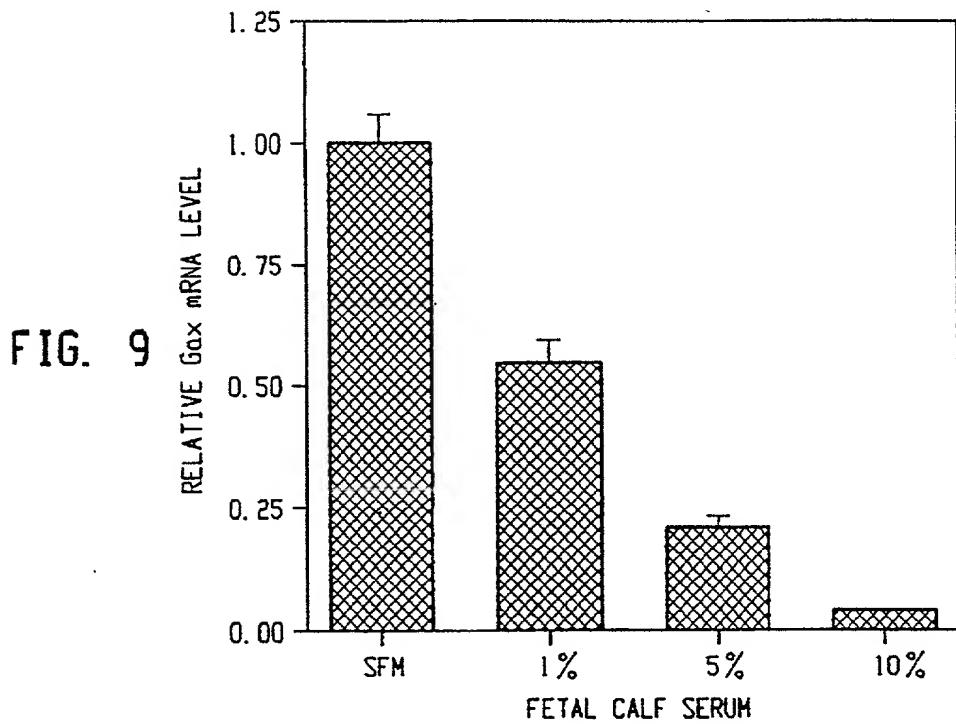


FIG. 9

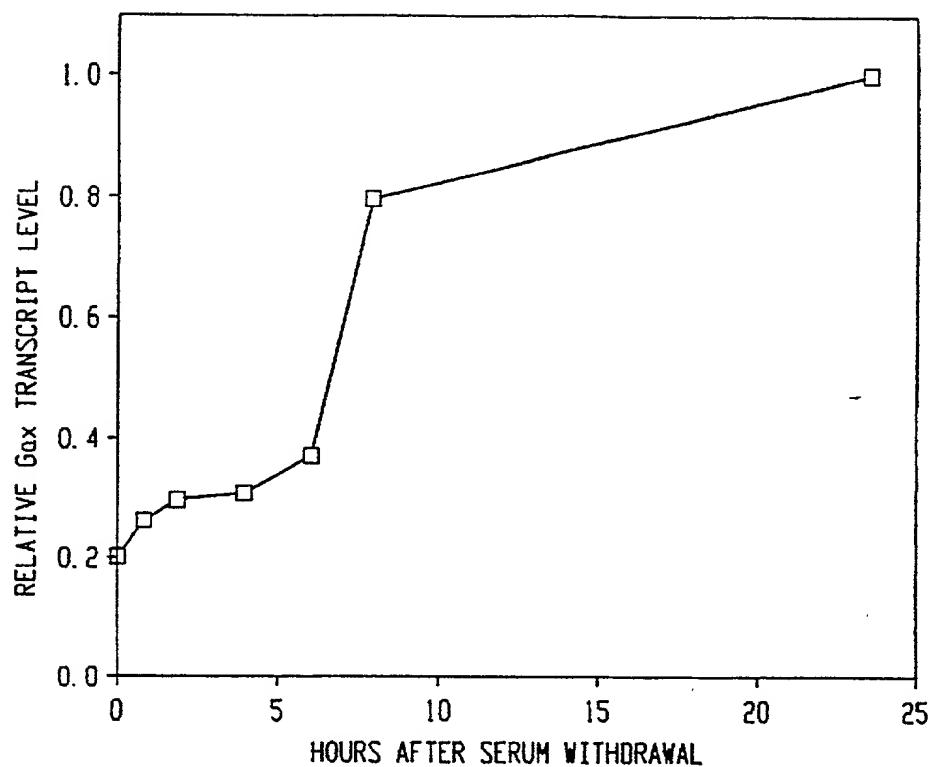


FIG. 10

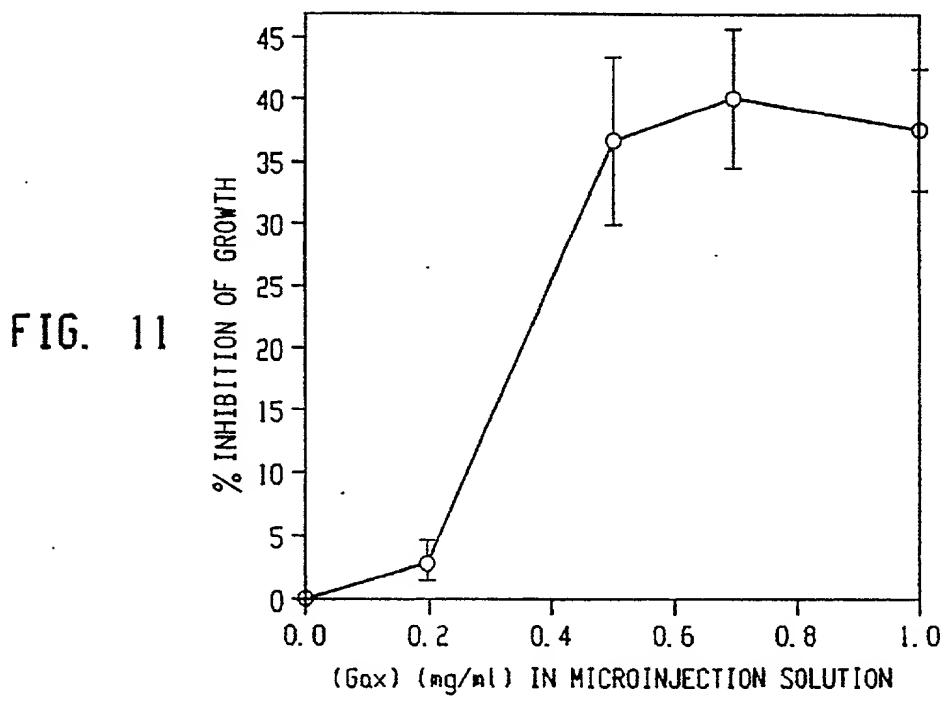


FIG. 11

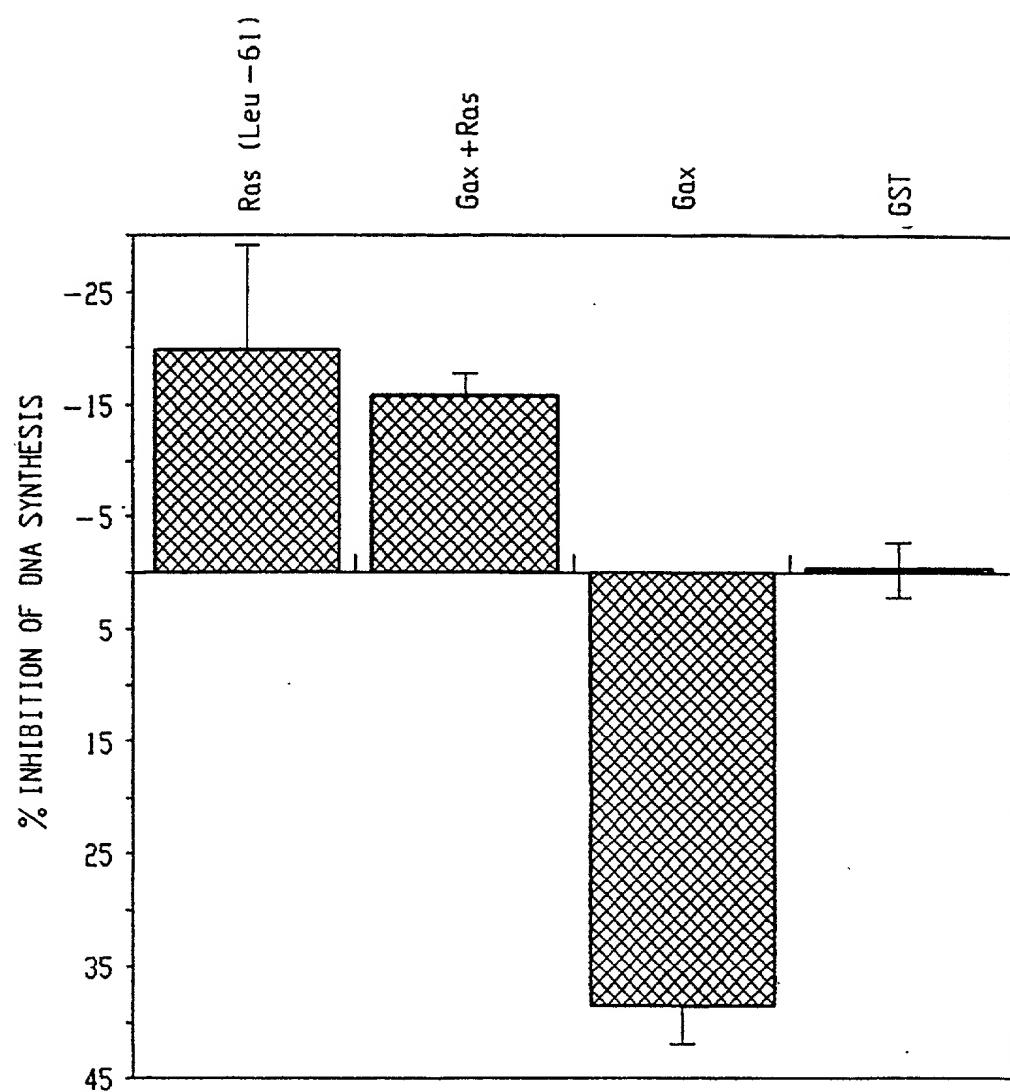


FIG. 12

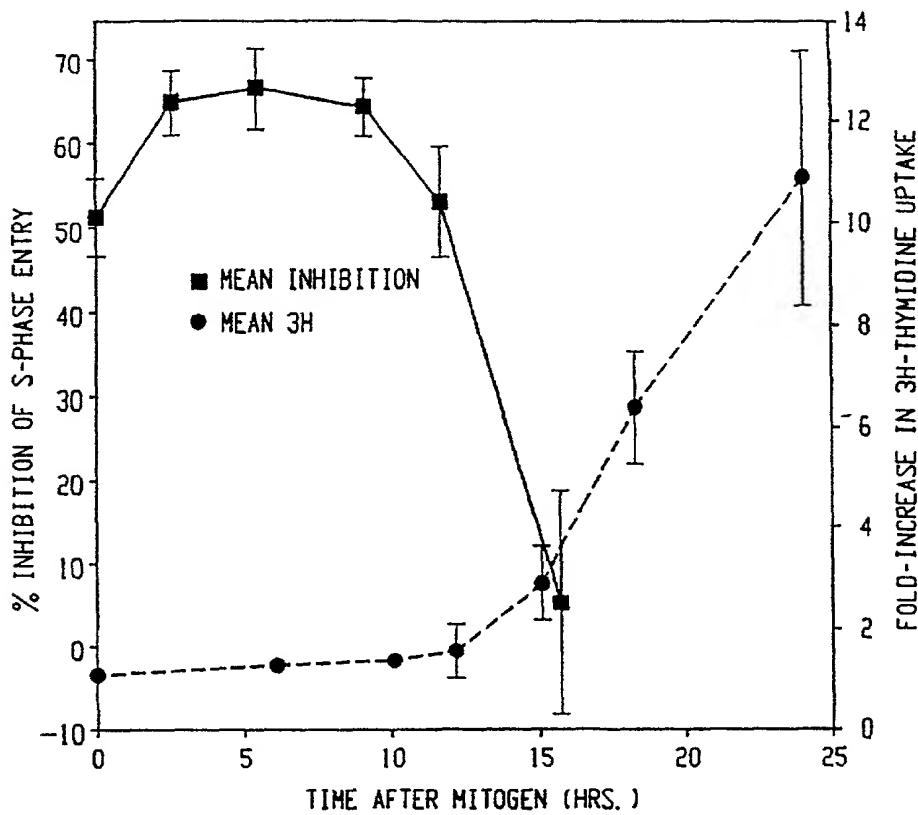


FIG. 13

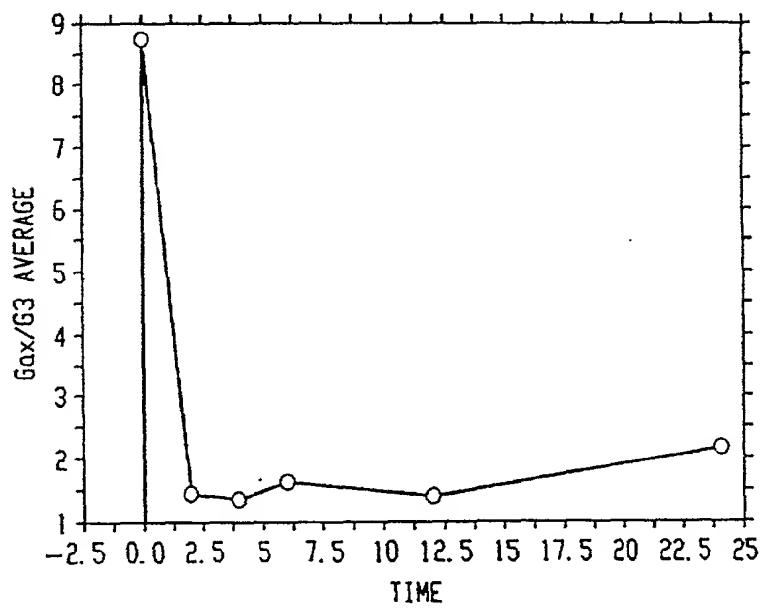


FIG. 14